

Figure S1. ASOs induce cleavage of nascent transcripts in vitro, Related to Figure 1 and Figure 5

(A) Genomic structure and subcellular localization of *NORAD*, *MALAT1*, *HOTAIR*, and *PPIB* transcripts. Locations targeted by ASOs indicated.

(B-E) qRT-PCR analysis of nascent transcript levels in NRO experiments in HCT116 (B-D) or HEK293T cells (E). The data come from the same experiment shown in Figures 1F-I and were analyzed in an identical manner except *B2M* was used to normalize transcript levels. ns, not significant; * $p<0.05$; ** $p<0.01$; calculated by Holm-Sidak's multiple comparison t test.

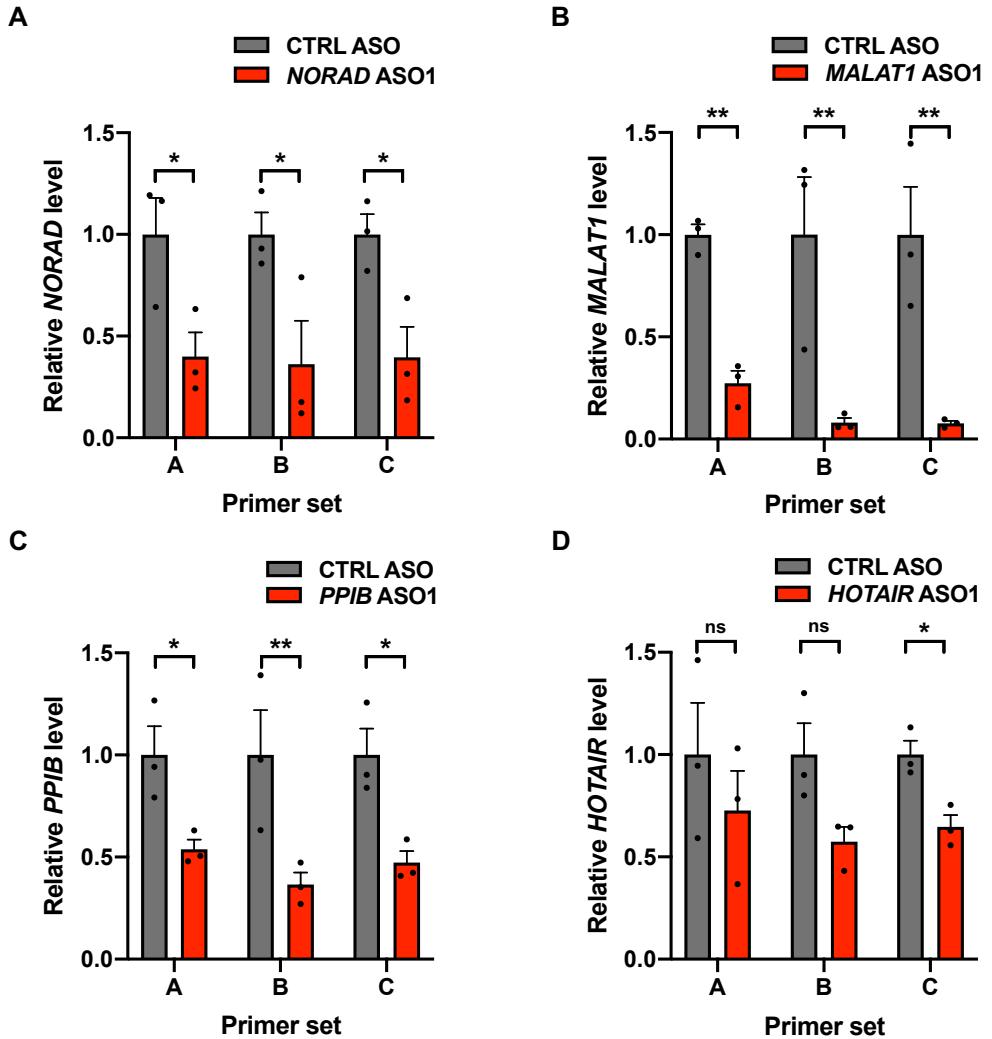


Figure S2. ASOs promote cleavage of chromatin-associated nascent transcripts in intact cells, Related to Figure 2

(A-D) qRT-PCR analysis of chromatin-associated nascent transcripts in HCT116 (A-C) or HEK293T cells (D). The data come from the same experiment shown in Figures 2B-E and were analyzed in an identical manner except *B2M* was used to normalize transcript levels. ns, not significant; *p<0.05; **p<0.01; calculated by Holm-Sidak's multiple comparison t test.

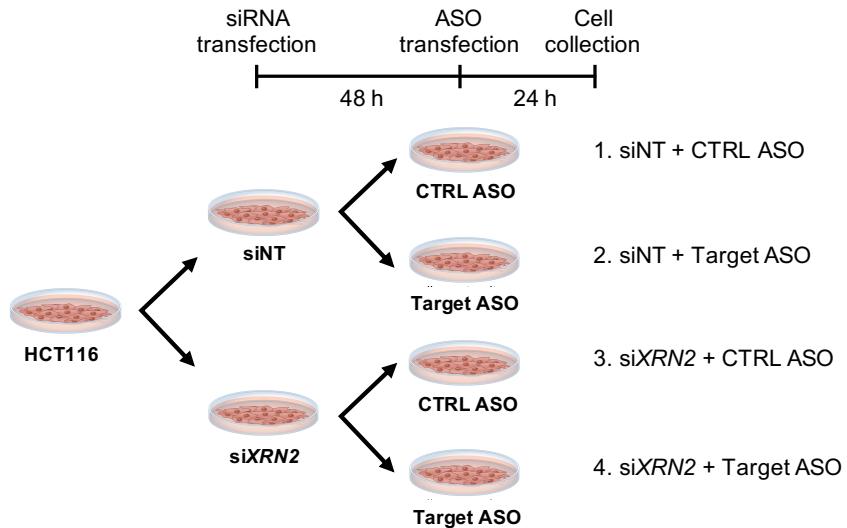
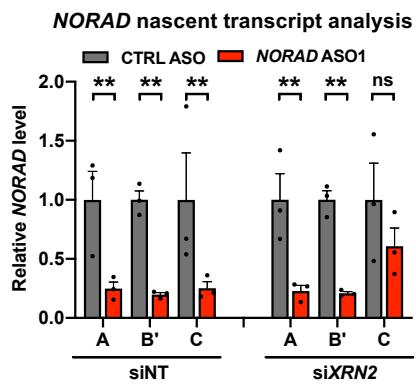
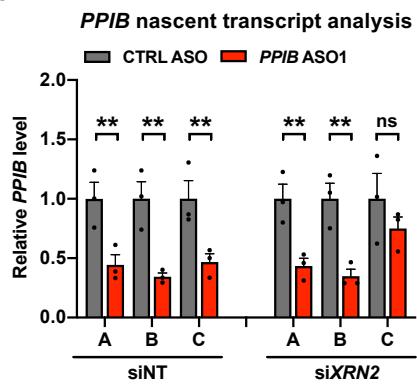
A**B****C**

Figure S3. Nascent transcript analysis following XRN2 knockdown and ASO transfection, Related to Figure 4

(A) Experimental design depicting transfection of HCT116 cells with control (siNT) or XRN2-targeting siRNA (siXRN2) followed by ASO transfection.

(B-C) qRT-PCR analysis of chromatin-associated nascent *NORAD* (B) or *PPIB* (C) transcripts following transfection of siRNA and ASOs. The data come from the same experiment shown in Figures 4B and 4E and were analyzed in an identical manner except *B2M* was used to normalize transcript levels. ns, not significant; **p<0.01; calculated by Holm-Sidak's multiple comparison t test.